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AMENDMENTS TO THE CLAIMS:

The following Listing of Claims will replace all prior listings, and version of claims in the application.

1. (Cancelled)

2. (Currently amended): A method of increasing the secretion of a heterologous protein in a eukaryotic cell comprising

inducing an unfolded protein response (UPR) by increasing the presence of a HAC1 UPR-modulating protein in said eukaryotic cell, comprising transforming the eukaryotic cell with a nucleic acid encoding the HAC1 UPR-modulating protein comprising a DNA binding domain having at least 90% sequence identity to a DNA binding domain of

a) amino acid residues 84 – 147 of SEQ ID NO: 5;

b) amino acid residues 53 – 116 of SEQ ID NO: 6 or

c) amino acid residues 45 – [[116]] 109 of SEQ ID No:19, and

increasing secretion of the heterologous protein relative to secretion of the heterologous protein in a parental cell.

3. (Original): The method of Claim 2 wherein said HAC1 protein is constitutively produced.

4. (Cancelled)

5. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from a cell selected from the group consisting of *Aspergillus, Trichoderma, Saccharomyces, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Fusarium, Neurospora,* and *Penicillium.*

6. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from yeast.

7. (Original): The method of Claim 6 wherein said yeast is *Saccharomyces cerevisiae.*

8. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from filamentous fungi.

9. (Original): The method of Claim 8 wherein said fungi is from *Trichoderma*.

10. (Original): The method of Claim 8 wherein said fungi is *Trichoderma reesei*.

11. (Original): The method of Claim 8 wherein said fungi is from *Aspergillus*.

12. (Original): The method of Claim 8 wherein said fungi is *Aspergillus nidulans*.

13. (Original): The method of Claim 8 wherein said fungi is *Aspergillus niger*.

14- 25. (Cancelled)

26. (Previously presented): The method of Claim 2 wherein said eukaryotic cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Schizosaccharomyces*, *Kluyveromyces*, *Pichia*, *Hansenula*, *Fusarium*, *Neurospora*, and *Penicillium*.

27. (Previously presented): The method of Claim 2 wherein said eukaryotic cell is a yeast cell.

28. (Original): The method of Claim 27 wherein said yeast is *Saccharomyces cerevisiae*.

29. (Previously presented): The method of Claim 2 wherein said eukaryotic cell is a filamentous fungi.

30. (Original): The method of Claim 29 wherein said fungi is from *Trichoderma*.

31. (Original): The method of Claim 29 wherein said fungi is *Trichoderma reesei*.

32. (Original): The method of Claim 29 wherein said fungi is from *Aspergillus*.

33. (Original): The method of Claim 29 wherein said fungi is *Aspergillus nidulans*.

34. (Original): The method of Claim 29 wherein said fungi is *Aspergillus niger*.

35. (Cancelled)

36. (Previously presented): The method of Claim 2 wherein said eukaryotic cell is a mammalian cell.

37-82. (Cancelled)

83. (Withdrawn) A cell containing a heterologous nucleic acid encoding a yeast or filamentous fungi protein having unfolded protein response modulating activity and a heterologous nucleic acid encoding a protein of interest to be secreted.

84. (Withdrawn): The cell of Claim 83 wherein said protein having unfolded protein response modulating activity is a fungal HAC1.

85. (Withdrawn): The cell of Claim 83 wherein said protein of interest is selected from the group consisting of lipase, cellulase, endo-glucosidase H, protease, carbohydrase, reductase, oxidase, isomerase, transferase, kinase, phosphatase, alpha-amylase, glucoamylase, ligtnocellulose hemicellulase, pectinase and ligninase.

86. (Cancelled)

87. (Withdrawn): The cell of Claim 83 wherein said protein having unfolded protein response modulating activity is a yeast HAC1.

88. (Cancelled):

89. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 90% identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5 or b) amino acid residues 53 – 116 of SEQ ID NO: 6.

90. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 95% identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID No: 5 or b) amino acid residues 53 – 116 of SEQ ID No: 6 or c) amino acid residues 45 – 116 of SEQ ID No:19.

91. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain having the DNA binding domain of amino acid residue positions 84 to 147 of SEQ ID NO: 5.

92. (Previously presented): The method of Claim 2 wherein said UPR-modulating protein comprises a DNA binding domain having the DNA binding domain of amino acid residue positions of 53 to 116 of SEQ ID NO: 6.

93. (Previously presented): The method of Claim 2, wherein said heterologous protein is selected from the group consisting of lipases, cellulases, endo-glucosidase H, proteases, carbohydrases, reductases, oxidases, isomerases, transferases, kinases, phosphatases, alpha-amylases, glucoamylases, hemicellulases, pectinases and ligninases.

94. (Previously presented): The method of Claim 93, wherein the heterologous protein is a protease, cellulase, glucoamylase or alpha amylase.

95. (Previously presented): The method of Claim 2, wherein the eukaryotic cell is a Trichoderma or Aspergillus fungal cell, the UPR-modulating protein comprising a DNA binding domain has at least 90% sequence identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5 or b) amino acid residues 53 – 116 of SEQ ID NO: 6 and the heterologous protein is selected from the group consisting of proteases, cellulases, glucoamylases, alpha amylases and combination thereof.

96. (Previously presented): The method of Claim 95, wherein the eukaryotic cell is a Trichoderma cell and the UPR-modulating protein comprises a DNA binding domain that has at least 95% sequence identity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5 or b) amino acid residues 53 – 116 of SEQ ID NO: 6.

97. (Previously presented): The method of Claim 95, wherein the eukaryotic cell is an Aspergillus cell and the UPR-modulating protein comprises a DNA binding domain that has at least 95% sequence similarity to the DNA binding domain of a) amino acid residues 84 – 147 of SEQ ID NO: 5; b) amino acid residues 53 – 116 of SEQ ID NO: 6.

98. (Previously presented): The method of Claim 2, further comprising a promoter operably linked to the nucleic acid encoding the HAC1 UPR-modulating protein, said promoter selected from the group consisting of *cbh*1, *gpd*A, *adh*1 and *pgk*1.